#41⁄48 12E12
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TO:	**Examiner Brian Whiteman**	FROM:	Donald Zuhn
COMPANY:	PTO Fax Center Crystal Mall 1; Group 1633	DATE:	June 4, 2001
FAX NUMBER:	703-305-7401	FIRM CODE:	349-118
PHONE NUMBER:		NO. OF PAGES:	9 (including cover page)

Re: Restriction Election Facsimile Transmission
U.S. Patent Application No. 09/729,264, filed November 28, 2000
"B7-Like Molecules and Uses Thereof"
Welcher *et al.*

60214512

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE
(Case No. 01,668)

PATENT

In re Application of: Welcher et al.   )
)
Serial No.:   09/729,264   ·)   Before the Examiner: B. Whiteman
)
Filed: November 28, 2000   )   Group Art Unit: 1633
)
For: B7-Like Molecules and Uses   )
       Thereof   )

Commissioner for Patents
Washington, D.C. 20231

Sir:

TRANSMITTAL LETTER

In regard to the above identified application:

1.   We are transmitting herewith the attached

      Response to Restriction Requirement

2.   Please charge any additional fees to Deposit Account No. 13-2490.

3.   The undersigned hereby certifies that this Transmittal Letter and this paper, as described in paragraph 1 herein above, are being facsimile transmitted to the Patent and Trademark Office (PTO Fax Center in Crystal Mall 1; Fax No. 703-305-7401) on June 4, 2001.

                                    Respectfully submitted,
                                    McDonnell Boehnen Hulbert & Berghoff

Dated: June 4, 2001   By: _____
                                    Donald Zuhn, Ph.D.
                                    Reg. No. P-48,710

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE
(Case No. 01,668)

PATENT

In re Application of: Welcher et al.   )
)
Serial No.:   09/729,264   )   Before the Examiner: B. Whiteman
)
Filed: November 28, 2000   )   Group Art Unit: 1633
)
For: B7-Like Molecules and Uses   )
       Thereof   )

Commissioner for Patents
Washington, D.C. 20231

Sir:

RESPONSE TO RESTRICTION REQUIREMENT
MAILED MAY 4, 2001

Responsive to the Restriction Requirement, mailed May 4, 2001, Applicants elect to prosecute claims 1-8, 10, 11, 46-48, and 55, designated as Group 1 by the Examiner. Applicants further elect to prosecute the species of the nucleic acid sequence as set forth in SEQ ID NO: 1, with traverse. The basis for Applicants' traversal of the requirement is as follows.

Applicants respectfully submit that there will be no undue hardship on the Office in performing a search with respect to the nucleic acid sequences of SEQ ID NOs: 1, 3, and 5. The putative secreted portion of the human B7-Like polypeptides encoded by these sequences (i.e., amino acid residues 9-382 of the amino acid sequence encoded by the nucleic acid sequence of SEQ ID NO: 1 and amino acid residues 13-386 of the amino acid sequences encoded by the nucleic acid sequences of SEQ ID NOs: 3 and 5) share a sequence identity of greater than 99% (Exhibit A). The open reading frames for each of these sequences share a sequence identity of greater than 97% (Exhibit B). Sequence alignments were performed using the application MacVector 7.0 (Accelrys, Cambridge, UK; http://www.accelrys.com) at the default settings.

Applicants do not believe any additional fee is required. However, the Commissioner is authorized to charge any deficiency to Deposit Account No. 13-2490. If Examiner Whiteman

believes it to be helpful, he is invited to contact the undersigned attorney by telephone at (312) 913-0001.

Respectfully submitted,
McDonnell Boehnen Hulbert & Berghoff

Dated: <u>June 4, 2001</u>

By: _____
Donald Zuhn, Ph.D.
Reg. No. P-48,710

EXHIBIT A

ClustalW (v1.4) multiple sequence alignment

3 Sequences Aligned   Alignment Score = 7182
Gaps Inserted = 0   Conserved Identities = 371

Pairwise Alignment Mode: Slow
Pairwise Alignment Parameters:
   Open Gap Penalty = 10.0   Extend Gap Penalty = 0.1
   Similarity Matrix: blosum

Multiple Alignment Parameters:
   Open Gap Penalty = 10.0   Extend Gap Penalty = 0.1
   Delay Divergent = 40%   Gap Distance = 8
   Similarity Matrix: blosum

Processing time: 0.9 seconds

```
SEQ05_AA     1 MERHLLTVPEAVGSGSGNEVIEGPQNATVLKGSQARFNCTVSQGWKLIMWALSDMVVLSVRPMEPIITND  70
SEQ03_AA     1 MVAGAMENRDPPGSGSGNEVIEGPQNARVLKGSQARFNCTVSQGWKLIMWALSDMVVLSVRPMEPIITND  70
SEQ01_AA     1         MGLVIFLHGSGSGNEVIEGPQNATVLKGSQARFNCTVSQGWKLIMWALSDMVVLSVRPMEPIITND  66
                        *********** ********************************************

SEQ05_AA    71 RFTSQRYDQGGNFTSEMIIHNVEPSDSGNIRCSLQNSRLHGSAYLTVQVMGELFIPSVNLVVAENEPCEV 140
SEQ03_AA    71 RFTSQRYDQGGNFTSEMIIHNVEPSDSGNIRCSLQNSRLHGSAYLTVQVMGELFIPSVNLVVAENEPCEV 140
SEQ01_AA    67 RFTSQRYDQGGNFTSEMIIHNVEPSDSGNIRCSLQNSRLHGSAYLTVQVMGELFIPSVNLVVAENEPCEV 136
               *********************************************************************

SEQ05_AA   141 TCLPSHWTRLPDISWELGLLVSHSSYYFVPEPSDLQSAVSILALTPQSNGTLTCVATWKSLKARKSATVN 210
SEQ03_AA   141 TCLPSHWTWLPDISWELGLLVSHSSYYFVPEPSDLQSAVSILALTPQSNGTLTCVATWKSLKARKSATVN 210
SEQ01_AA   137 TCLPSHWTRLPDISWELGLLVSHSSYYFVPEPSDLQSAVSILALTPQSNGTLTCVATWKSLKARKSATVN 206
               ******** ************************************************************

SEQ05_AA   211 LTVIRCPQDTGGGINIPGVLSSLPSLGPSLPTWGKVGLGLAGTMLLTPTCTLTIRCCCCRRRCCGCNCCC 280
SEQ03_AA   211 LTVIRCPQDTGGGINIPGVLSSLPSLGFSLPTWGKVGLGLAGTMLLTPTCTLTIRCCCCRRRCCGCNCCC 280
SEQ01_AA   207 LTVIRCPQDTGGGINIPGVLSSLPSLGFSLPTWGKVGLGLAGTMLLTPTCTLTIRCCCCRRRCCGCNCCC 276
               *********************************************************************

SEQ05_AA   281 RCCFCCRRKRGFRIQFQKKSEKEKTNKETETESGNENSGYNSDEQKTTETASLPPKSCESSDPEQRNSSC 350
SEQ03_AA   281 RCCFCCRRKRGFRIQFQKKSEKEKTNKETETESGNENSGVNSDEQKTTDTASLPPKSCESSDPEQRNSSC 350
SEQ01_AA   277 RCCFCCRRKRGFRIQFQKKSEKEKTNKETETESGNENSGYNSDEQKTTDTASLPPKSCESSDPEQRNSSC 346
               **************************************** *****************************

SEQ05_AA   351 GPPHQRADQRPPRPASHPQASFNLASPEKVSNTTVV 386
SEQ03_AA   351 GPPHQRADQRPPRPASHPQASFNLASPEKVSNTTVV 386
SEQ01_AA   347 GPPHQRADQRPPRPASHPQASFNLASPEKVSNTTVV 382
               ************************************
```

EXHIBIT B

Nucleic acid sequence alignment for SEQ ID NO: 1, 3, and 5 open reading frames.

Search Analysis for Sequence: SEQ01_ORF   Matrix: DNA database matrix
Search from 1 to 1146 where origin = 1   Score Region from 1 to 1146
Date: June 4, 2001   Maximum possible score: 4584
Time: 16:32:55

Database: Folder 'untitled folder'

```
                  10        20        30        40        50        60        70
SEQ01_ORF    atggggcttgtgattttcctccacggttctgggtctggtaatgaagtcatagaaggcccccagaatgcaa

1. SEQ03_ORF   20        30        40        50        60        70        80
[ 4488 ]     ATGGAAAAT-AGA-GACCCACC-CGGTTCTGGGTCTGGTAATGAAGTCATAGAAGGCCCCCAAAATGCAA>
             ||||   |  ||     ||  || |||||||||||||||||||||||||||||||||||||||| |||||||
SEQ01_ORF    atggggcttgtgattttcctccacggttctgggtctggtaatgaagtcatagaaggcccccagaatgcaa

2. SEQ05_ORF                       40        50        60        70        80
[ 4486 ]                 CTGTA-GGTTCTGGGTCTGGTAATGAAGTCATAGAAGGCCCCCAGAATGCAA>
                         || |  |||||||||||||||||||||||||||||||||||||||||||||||
SEQ01_ORF                ctccacggttctgggtctggtaatgaagtcatagaaggcccccagaatgcaa


                  80        90        100       110       120       130       140
SEQ01_ORF    cagtcctgaagggctcccaggctcgcttcaactgcaccgtctcccagggctggaagctcatcatgtgggc

1. SEQ03_ORF   90        100       110       120       130       140       150
[ 4488 ]     GAGTCCTGAAGGGCTCCCAGGCTCGCTTCAACTGCACCGTCTCCCAGGGCTGGAAGCTCATCATGTGGGC>
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SEQ01_ORF    cagtcctgaagggctcccaggctcgcttcaactgcaccgtctcccagggctggaagctcatcatgtgggc

2. SEQ05_ORF   90        100       110       120       130       140       150
[ 4486 ]     CAGTCCTGAAGGGCTCCCAGGCTCGCTTCAACTGCACCGTCTCCCAGGGCTGGAAGCTCATCATGTGGGC>
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SEQ01_ORF    cagtcctgaagggctcccaggctcgcttcaactgcaccgtctcccagggctggaagctcatcatgtgggc


                  150       160       170       180       190       200       210
SEQ01_ORF    tctcagtgacatggtggtgctaagcgtcaggcccatggagcccatcatcaccaatgaccgcttcacctct

1. SEQ03_ORF   160       170       180       190       200       210       220
[ 4488 ]     TCTCAGTGACATGGTGGTGCTAAGCGTCAGGCCCATGGAGCCCATCATCACCAATGACCGCTTCACCTCT>
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SEQ01_ORF    tctcagtgacatggtggtgctaagcgtcaggcccatggagcccatcatcaccaatgaccgcttcacctct

2. SEQ05_ORF   160       170       180       190       200       210       220
[ 4486 ]     TCTCAGTGACATGGTGGTGCTAAGCGTCAGGCCCATGGAGCCCATCATCACCAATGACCGCTTCACCTCT>
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SEQ01_ORF    tctcagtgacatggtggtgctaagcgtcaggcccatggagcccatcatcaccaatgaccgcttcacctct


                  220       230       240       250       260       270       280
SEQ01_ORF    cagaggtacgaccagggcgggaacttcacctcggagatgatcatccacaatgtggagcccagtgattcgg

1. SEQ03_ORF   230       240       250       260       270       280       290
[ 4488 ]     CAGAGGTACGACCAGGGCGGGAACTTCACCTCGGAGATGATCATCCACAATGTGGAGCCCAGTGATTCGG>
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SEQ01_ORF    cagaggtacgaccagggcgggaacttcacctcggagatgatcatccacaatgtggagcccagtgattcgg

2. SEQ05_ORF   230       240       250       260       270       280       290
[ 4486 ]     CAGAGGTACGACCAGGGCGGGAACTTCACCTCGGAGATGATCATCCACAATGTGGAGCCCAGTGATTCGG>
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SEQ01_ORF    cagaggtacgaccagggcgggaacttcacctcggagatgatcatccacaatgtggagcccagtgattcgg
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1

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                    290       300       310       320       330       340       350
SEQ01_ORF    ggaacatcagatgcagcctccagaacagtcgcctgcatggatctgcttaccttaccgtccaagttatggg

                    300       310       320       330       340       350       360
1. SEQ03_ORF   GGAACATCAGATGCAGCCTCCAGAACAGTCGCCTGCATGGATCTGCTTACCTTACCGTCCAAGTTATGGG>
[ 4488 ]       |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SEQ01_ORF      ggaacatcagatgcagcctccagaacagtcgcctgcatggatctgcttaccttaccgtccaagttatggg

                    300       310       320       330       340       350       360
2. SEQ05_ORF   GGAACATCAGATGCAGCCTCCAGAACAGTCGCCTGCATGGATCTGCTTACCTTACCGTCCAAGTTATGGG>
[ 4486 ]       |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SEQ01_ORF      ggaacatcagatgcagcctccagaacagtcgcctgcatggatctgcttaccttaccgtccaagttatggg


                    360       370       380       390       400       410       420
SEQ01_ORF    agagctgttcattcccagtgttaatcttgtagtcgctgagaatgaaccttgtgaagttacttgtctaccc

                    370       380       390       400       410       420       430
1. SEQ03_ORF   AGAGCTGTTCATTCCCAGTGTTAATCTTGTAGTCGCTGAGAATGAACCTTGTGAAGTTACTTGTCTACCC>
[ 4488 ]       |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SEQ01_ORF      agagctgttcattcccagtgttaatcttgtagtcgctgagaatgaaccttgtgaagttacttgtctaccc

                    370       380       390       400       410       420       430
2. SEQ05_ORF   AGAGCTGTTCATTCCCAGTGTTAATCTTGTAGTCGCTGAGAATGAACCTTGTGAAGTTACTTGTCTACCC>
[ 4486 ]       |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SEQ01_ORF      agagctgttcattcccagtgttaatcttgtagtcgctgagaatgaaccttgtgaagttacttgtctaccc


                    430       440       450       460       470       480       490
SEQ01_ORF    tcacactggacccggctcccggatatttcctgggagctcggtctcctggtcagccattcaagctattatt

                    440       450       460       470       480       490       500
1. SEQ03_ORF   TCACACTGGACCTGGCTCCCGGATATTTCCTGGGAGCTCGGTCTCCTGGTCAGCCATTCAAGCTATTATT>
[ 4488 ]       ||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SEQ01_ORF      tcacactggacccggctcccggatatttcctgggagctcggtctcctggtcagccattcaagctattatt

                    440       450       460       470       480       490       500
2. SEQ05_ORF   TCACACTGGACCCGGCTCCCGGATATTTCCTGGGAGCTCGGTCTCCTGGTCAGCCATTCAAGCTATTATT>
[ 4486 ]       |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SEQ01_ORF      tcacactggacccggctcccggatatttcctgggagctcggtctcctggtcagccattcaagctattatt


                    500       510       520       530       540       550       560
SEQ01_ORF    ttgttccggagcccagcgaccttcaaagtgcagtgagcatcctggctctgacccacagagcaatgggac

                    510       520       530       540       550       560       570
1. SEQ03_ORF   TTGTTCCGGAGCCCAGCGACCTTCAAAGTGCAGTGAGCATCCTGGCTCTGACCCCACAGAGCAATGGGAC>
[ 4488 ]       ||||||||||||||||||||||||||||||  |||||||||||||||||||||  ||||||||||||||||
SEQ01_ORF      ttgttccggagcccagcgaccttcaaagtgcagtgagcatcctggctctgaccccacagagcaatgggac

                    510       520       530       540       550       560       570
2. SEQ05_ORF   TTGTTCCGGAGCCCAGCGACCTTCAAAGTGCAGTGAGCATCCTGGCTCTGACCCCACAGAGCAATGGGAC>
[ 4486 ]       ||||||||||||||||||||||||||||||  |||||||||||||||||||||  ||||||||||||||||
SEQ01_ORF      ttgttccggagcccagcgaccttcaaagtgcagtgagcatcctggctctgacccacagagcaatgggac


                    570       580       590       600       610       620       630
SEQ01_ORF    tttgacttgcgtggctacctggaagagcctgaaggcccgcaagtctgcaactgtaaatctcactgtgatt

                    580       590       600       610       620       630       640
1. SEQ03_ORF   TTTGACTTCCCTCCCTACCTGGAAGAGCCTGAAGGCCCGCAAGTCTGCAACTGTAAATCTCACTGTGATT>
[ 4488 ]       ||||||||  | || |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SEQ01_ORF      tttgacttgcgtggctacctggaagagcctgaaggcccgcaagtctgcaactgtaaatctcactgtgatt

                    580       590       600       610       620       630       640
2. SEQ05_ORF   TTTGACTTCCCTCCCTACCTGGAAGAGCCTGAAGGCCCGCAAGTCTGCAACTGTAAATCTCACTGTGATT>
[ 4486 ]       ||||||||  | || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SEQ01_ORF      tttgacttgcgtggctacctggaagagcctgaaggcccgcaagtctgcaactgtaaatctcactgtgatt
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2

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                    640       650       660       670       680       690       700
SEQ01_ORF   cggtgtccccaagacactggaggtggtattaatattccaggtgtattatcaagtttaccgagtttaggtt

                    650       660       670       680       690       700       710
1. SEQ03_ORF        CGGTGTCCCCAAGACACTGGAGGTGGTATTAATATTCCAGGTGTATTATCAAGTTTACCGAGTTTAGGTT>
[ 4488 ]            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SEQ01_ORF           cggtgtccccaagacactggaggtggtattaatattccaggtgtattatcaagtttaccgagtttaggtt

                    650       660       670       680       690       700       710
2. SEQ05_ORF        CGGTGTCCCCAAGACACTGGAGGTGGTATTAATATTCCAGGTGTATTATCAAGTTTACCGAGTTTAGGTT>
[ 4486 ]            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SEQ01_ORF           cggtgtccccaagacactggaggtggtattaatattccaggtgtattatcaagtttaccgagtttaggtt


                    710       720       730       740       750       760       770
SEQ01_ORF   tttcattgcctacttggggcaaagttggacttggactagcaggcaccatgcttctgacgccgacgtgtac

                    720       730       740       750       760       770       780
1. SEQ03_ORF        TTTCATTGCCTACTTGGGGCAAAGTTGGACTTGGACTAGCAGGCACCATGCTTCTGACGCCGACGTGTAC>
[ 4488 ]            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SEQ01_ORF           tttcattgcctacttggggcaaagttggacttggactagcaggcaccatgcttctgacgccgacgtgtac

                    720       730       740       750       760       770       780
2. SEQ05_ORF        TTTCATTGCCTACTTGGGGCAAAGTTGGACTTGGACTAGCAGGCACCATGCTTCTGACGCCGACGTGTAC>
[ 4486 ]            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SEQ01_ORF           tttcattgcctacttggggcaaagttggacttggactagcaggcaccatgcttctgacgccgacgtgtac


                    780       790       800       810       820       830       840
SEQ01_ORF   tcttacaatacgctgctgctgctgccgccgtcgttgttgtggctgcaactgctgctgccgttgttgtttc

                    790       800       810       820       830       840       850
1. SEQ03_ORF        TCTTACAATACGCTGCTGCTGCTGCCGCCGTCGTTGTTGTGGCTGCAACTGCTGCTGCCGTTGTTGTTTC>
[ 4488 ]            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SEQ01_ORF           tcttacaatacgctgctgctgctgccgccgtcgttgttgtggctgcaactgctgctgccgttgttgtttc

                    790       800       810       820       830       840       850
2. SEQ05_ORF        TCTTACAATACGCTGCTGCTGCTGCCGCCGTCGTTGTTGTGGCTGCAACTGCTGCTGCCGTTGTTGTTTC>
[ 4486 ]            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SEQ01_ORF           tcttacaatacgctgctgctgctgccgccgtcgttgttgtggctgcaactgctgctgccgttgttgtttc


                    850       860       870       880       890       900       910
SEQ01_ORF   tgctgtagaagaaaaagaggatttcgtattcaatttcaaaagaaatctgaaaaagagaagacaaacaaag

                    860       870       880       890       900       910       920
1. SEQ03_ORF        TGCTGTAGAAGAAAAAGAGGATTTCGTATTCAATTTCAAAAGAAATCTGAAAAAGAGAAGACAAACAAAG>
[ 4488 ]            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SEQ01_ORF           tgctgtagaagaaaaagaggatttcgtattcaatttcaaaagaaatctgaaaaagagaagacaaacaaag

                    860       870       880       890       900       910       920
2. SEQ05_ORF        TGCTGTAGAAGAAAAAGAGGATTTCGTATTCAATTTCAAAAGAAATCTGAAAAAGAGAAGACAAACAAAG>
[ 4486 ]            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SEQ01_ORF           tgctgtagaagaaaaagaggatttcgtattcaatttcaaaagaaatctgaaaaagagaagacaaacaaag


                    920       930       940       950       960       970       980
SEQ01_ORF   aaactgagacagaaagtggaaatgaaaactccggctacaattcagatgaacaaaagaccacagacaccgc

                    930       940       950       960       970       980       990
1. SEQ03_ORF        AAACTGAGACAGAAAGTGGAAATGAAAACTCCGGCTACAATTCAGATCAACAAAACACCACACACACCCC>
[ 4488 ]            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SEQ01_ORF           aaactgagacagaaagtggaaatgaaaactccggctacaattcagatgaacaaaagaccacagacaccgc

                    930       940       950       960       970       980       990
2. SEQ05_ORF        AAACTCACACAGAAAGTGGAAATGAAAACTCCGGCTACAATTCAGATGAACAAAAGACCCACAGAAACCCC-
[ 4486 ]            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
SEQ01_ORF           aaactgagacagaaagtggaaatgaaaactccggctacaattcagatgaacaaaagaccacagacaccgc
```

3

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                  990       1000      1010      1020      1030      1040      1050
SEQ01_ORF    ttctctccctcccaaatcctgtgaatccagtgatcctgaacaaagaaacagtagctgtggccctcctcac

                  1000      1010      1020      1030      1040      1050      1060
1. SEQ03_ORF
[ 4488 ]     TTCTCTCCCTCCCAAATCCTGTGAATCCAGTGATCCTGAACAAAGAAACAGTAGCTGTGGCCCTCCTCAC>
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SEQ01_ORF    ttctctccctcccaaatcctgtgaatccagtgatcctgaacaaagaaacagtagctgtggccctcctcac

                  1000      1010      1020      1030      1040      1050      1060
2. SEQ05_ORF
[ 4486 ]     TTCTCTCCCTCCCAAATCCTGTGAATCCAGTGATCCTGAACAAAGAAACAGTAGCTGTGGCCCTCCTCAC>
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SEQ01_ORF    ttctctccctcccaaatcctgtgaatccagtgatcctgaacaaagaaacagtagctgtggccctcctcac

                  1060      1070      1080      1090      1100      1110      1120
SEQ01_ORF    cagcgggctgatcaacgtccacccaggccagcaagtcatccacaggcttcttttaatctggccagtcctg

                  1070      1080      1090      1100      1110      1120      1130
1. SEQ03_ORF
[ 4488 ]     CAGCGGGCTGATCAACGTCCACCCAGGCCAGCAAGTCATCCACAGGCTTCTTTTAATCTGGCCAGTCCTG>
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SEQ01_ORF    cagcgggctgatcaacgtccacccaggccagcaagtcatccacaggcttcttttaatctggccagtcctg

                  1070      1080      1090      1100      1110      1120      1130
2. SEQ05_ORF
[ 4486 ]     CAGCGGGCTGATCAACGTCCACCCAGGCCAGCAAGTCATCCACAGGCTTCTTTTAATCTGGCCAGTCCTG>
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SEQ01_ORF    cagcgggctgatcaacgtccacccaggccagcaagtcatccacaggcttcttttaatctggccagtcctg

                  1130      1140
SEQ01_ORF    agaaggtcagtaatacaactgtagta

                  1140      1150
1. SEQ03_ORF
[ 4488 ]     AGAAGGTCAGTAATACAACTGTAGTA>
             ||||||||||||||||||||||||||
SEQ01_ORF    agaaggtcagtaatacaactgtagta

                  1140      1150
2. SEQ05_ORF
[ 4486 ]     AGAAGGTCAGTAATACAACTGTAGTA>
             ||||||||||||||||||||||||||
SEQ01_ORF    agaaggtcagtaatacaactgtagta
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4